0606

#5

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/032,256A

DATE: 06/03/2002
TIME: 13:22:15

Input Set : A:\M2335hn1.app
Output Set: N:\CRF3\06032002\J032256A.raw

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  3 <110> APPLICANT: CHODOSH, Lewis A
  4       GARDNER, Heather P
  6 <120> TITLE OF INVENTION: HORMONALLY UP-REGULATED, NEU-TUMOR-ASSOCIATED KINASE
  8 <130> FILE REFERENCE: 22253-70421
 10 <140> CURRENT APPLICATION NUMBER: 10/032,256A
C--> 11 <141> CURRENT FILING DATE: 2002-05-21
 13 <150> PRIOR APPLICATION NUMBER: 60/257,073
 14 <151> PRIOR FILING DATE: 2000-12-21
 16 <160> NUMBER OF SEQ ID NOS: 18
 18 <170> SOFTWARE: PatentIn Ver. 2.1
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 21 <211> LENGTH: 5024
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Murinae gen. sp.
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 32 gagccaagaa agacacctac gtcaccaaaa acctgcgtcg agaggggcag atccagcaga 420
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 36 tgcaccgtgc gggggtggtt cacagagact tgaagataga gaatttgcta ctagatgaag 660
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106 tcatgaatga gtctttgcct gtgattctag tcagcctgtg gctactgatg ggaacggccg 4860
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122              20                  25                  30
124 Glu Gly Ser Phe Leu Pro Ala Trp Val Ser Gly Val Ser Arg Glu Arg
125          35                  40                  45
127 Leu Arg Asp Phe Gln His His Lys Arg Val Gly Asn Tyr Leu Ile Gly
128      50                  55                  60
130 Ser Arg Lys Leu Gly Glu Gly Ser Phe Ala Lys Val Arg Glu Gly Leu
131  65                  70                  75                  80
133 His Val Leu Thr Gly Glu Lys Val Ala Ile Lys Val Ile Asp Lys Lys
134                  85                  90                  95
136 Arg Ala Lys Lys Asp Thr Tyr Val Thr Lys Asn Leu Arg Arg Glu Gly
137              100                 105                 110
139 Gln Ile Gln Gln Met Ile Arg His Pro Asn Ile Thr Gln Leu Leu Asp
140          115                 120                 125
142 Ile Leu Glu Thr Glu Asn Ser Tyr Tyr Leu Val Met Glu Leu Cys Pro
143      130                 135                 140
145 Gly Gly Asn Leu Met His Lys Ile Tyr Glu Lys Lys Arg Leu Asp Glu
146 145                 150                 155                 160
148 Ala Glu Ala Arg Arg Tyr Ile Arg Gln Leu Ile Ser Ala Val Glu His
149                 165                 170                 175
151 Leu His Arg Ala Gly Val Val His Arg Asp Leu Lys Ile Glu Asn Leu
152              180                 185                 190
154 Leu Leu Asp Glu Asp Asn Asn Ile Lys Leu Ile Asp Phe Gly Leu Ser
155          195                 200                 205
157 Asn Cys Ala Gly Ile Leu Gly Tyr Ser Asp Pro Phe Ser Thr Gln Cys
158      210                 215                 220
160 Gly Ser Pro Ala Tyr Ala Ala Pro Glu Leu Leu Ala Arg Lys Lys Tyr
161 225                 230                 235                 240
163 Gly Pro Lys Ile Asp Val Trp Ser Ile Gly Val Asn Met Tyr Ala Met
164                 245                 250                 255
166 Leu Thr Gly Thr Leu Pro Phe Thr Val Glu Pro Phe Ser Leu Arg Ala
167              260                 265                 270
169 Leu Tyr Gln Lys Met Val Asp Lys Ala Met Asn Pro Leu Pro Thr Gln
170          275                 280                 285
172 Leu Ser Thr Gly Ala Val Asn Phe Leu Arg Ser Leu Leu Glu Pro Asp
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Output Set: N:\CRF3\06032002\J032256A.raw

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178 Asn Glu Asn Tyr Thr Gly Lys Val Pro Cys Asn Val Thr Tyr Pro Asn
179                 325                 330                 335
181 Arg Ile Ser Leu Glu Asp Leu Ser Pro Ser Val Val Leu His Met Thr
182             340                 345                 350
184 Glu Lys Leu Gly Tyr Lys Asn Ser Asp Val Ile Asn Thr Val Leu Ser
185         355                 360                 365
187 Asn Arg Ala Cys His Ile Leu Ala Ile Tyr Phe Leu Leu Asn Lys Lys
188     370                 375                 380
190 Leu Glu Arg Tyr Leu Ser Gly Lys Ser Asp Ile Gln Asp Ser Ile Cys
191 385                 390                 395                 400
193 Tyr Lys Thr Gln Leu Tyr Gln Ile Glu Lys Cys Arg Ala Thr Lys Glu
194                 405                 410                 415
196 Pro Tyr Glu Ala Ser Leu Asp Thr Trp Thr Arg Asp Phe Glu Phe His
197             420                 425                 430
199 Ala Val Gln Asp Lys Lys Pro Lys Glu Gln Glu Lys Arg Gly Asp Phe
200         435                 440                 445
202 Leu His Arg Pro Phe Ser Lys Lys Leu Asp Lys Asn Leu Pro Ser His
203     450                 455                 460
205 Lys Gln Pro Ser Pro Ser Leu Ile Thr Gln Leu Gln Ser Thr Lys Ala
206 465                 470                 475                 480
208 Leu Leu Lys Asp Arg Lys Ala Ser Lys Ser Gly Phe Pro Asp Lys Asp
209                 485                 490                 495
211 Ser Phe Val Cys Arg Asn Leu Phe Arg Lys Thr Ser Asp Ser Asn Cys
212             500                 505                 510
214 Val Ala Ser Ser Ser Met Glu Phe Ile Pro Val Pro Pro Pro Arg Thr
215         515                 520                 525
217 Pro Arg Ile Val Lys Lys Leu Glu Pro His Gln Pro Gly Pro Gly Ser
218     530                 535                 540
220 Ala Ser Ile Leu Pro Lys Glu Glu Pro Leu Leu Leu Asp Met Val Arg
221 545                 550                 555                 560
223 Ser Phe Glu Ser Val Asp Arg Glu Asp His Ile Glu Leu Leu Ser Pro
224                 565                 570                 575
226 Ser His His Tyr Arg Ile Leu Ser Ser Pro Val Ser Leu Ala Arg Arg
227             580                 585                 590
229 Asn Ser Ser Glu Arg Thr Leu Ser Gln Gly Leu Leu Ser Gly Ser Thr
230         595                 600                 605
232 Ser Pro Leu Gln Thr Pro Leu His Ser Thr Leu Val Ser Phe Ala His
233     610                 615                 620
235 Glu Glu Lys Asn Ser Pro Pro Lys Glu Glu Gly Val Cys Ser Pro Pro
236 625                 630                 635                 640
238 Pro Val Pro Ser Asn Gly Leu Leu Gln Pro Leu Gly Ser Pro Asn Cys
239                 645                 650                 655
241 Val Lys Ser Arg Gly Arg Phe Pro Met Met Gly Ile Gly Gln Met Leu
242             660                 665                 670
244 Arg Lys Arg His Gln Ser Leu Gln Pro Ser Ser Glu Arg Ser Leu Asp
245         675                 680                 685
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255 <211> LENGTH: 10
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257 <213> ORGANISM: Unknown Organism
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260 <223> OTHER INFORMATION: Description of Unknown Organism:Kozak consensus
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268 <211> LENGTH: 6
269 <212> TYPE: DNA
270 <213> ORGANISM: Unknown Organism
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Unknown Organism:polyadenylation
274       signal
276 <400> SEQUENCE: 4
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281 <211> LENGTH: 6
282 <212> TYPE: DNA
283 <213> ORGANISM: Murinae gen. sp.
285 <400> SEQUENCE: 5
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290 <211> LENGTH: 6
291 <212> TYPE: PRT
292 <213> ORGANISM: murine Hunk;fragment
294 <400> SEQUENCE: 6
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296   1               5
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300 <211> LENGTH: 21
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <221> NAME/KEY: misc_feature
306 <222> LOCATION: (17)
307 <223> OTHER INFORMATION: n is a, c, g, or t
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310 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
311       oligonucleotide primer PTKIa
313 <400> SEQUENCE: 7
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317 <210> SEQ ID NO: 8
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 17